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microRNA Bioinformatics

Guest Editor:

Prof. Dr. Y-h. Taguchi

Department of Physics, Chuo
University, Tokyo 112-8551,
Japan

Deadline for manuscript
submissions:

closed (31 October 2020)

Message from the Guest Editor

Dear Colleagues,

Numerous computational methods have been proposed for studying the highly context-dependent interaction between miRNAs and mRNAs. Various databases for storing this information are continuously being established, and more and more applications are required for identifying new miRNAs in various species. In contrast to proteins and protein-coding RNAs, miRNAs have a greater potential to be targeted by computational methods. For this Special Issue, all kinds of studies related to the development of databases and applications, and investigations of miRNAs using existing applications are encouraged.

Prof. Y-h. Taguchi

Guest Editor



mdpi.com/si/28280

Special Issue



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Contact Us

Cells Editorial Office
MDPI, Grosspeteranlage 5
4052 Basel, Switzerland

Tel: +41 61 683 77 34
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